Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application.

Claims 1-22 (canceled)

Claim 23 (currently amended): A method for the diagnosis or prognosis of an immune pathology by quantitative evaluation of a rearrangement of the T-cell Receptor alpha/delta (TCRAD) locus of a human individual which method comprises at least:

(a) extracting human genomic DNA from a biological sample of said individual, selected from ~~in~~ the group consisting of blood and biopsies;

(b) amplifying multiple different segments ~~a long segment~~ of said genomic DNA (gDNA) resulting from different VJ rearrangements ~~comprising at least a few hundred base pairs, by multiplex long PCR,~~ of the genes of the TCRAD locus ~~TCRAD, said amplifying being~~ , wherein said amplification is performed by multiplex PCR, in the presence:

(i) of one or more pairs of primers, wherein at least one of said pairs of primers consists ~~consisting~~ of:

- a first primer called primer V, said primer V hybridizing specifically with a region located upstream of the RSS sequence of a Vx gene to be amplified or with the 5' end of said Vx gene, said Vx gene encoding a V segment of the variable domain of the α chain of a T-cell receptor (TCRAD);

-a second primer, called primer J, said primer J hybridizing specifically with a region located downstream of the RSS sequence of a Jy gene to be amplified, or with the 3' end of said Jy gene to be amplified or in said Jy gene to be amplified, said Jy gene encoding a J segment of the α chain of a T-cell receptor;

(ii) and of a DNA polymerase or a mixture of DNA polymerases for amplifying ~~long~~ genomic DNA segments, and having a correction activity;

said ~~amplifying~~ amplification comprising, in addition to the initial denaturation step, cycles of denaturation, hybridization and elongation, in which the elongation steps are carried out at least for 10 minutes at 68°C - 72°C;

(c) separating the amplified gDNA fragments by electrophoretic migration on a gel, in the presence of a DNA-labeling agent, and

(d) detecting the rearranged VJ segments directly on the gel, ~~and detecting~~ after excitation in the UV range or at another appropriate wavelength.

Claim 24 (currently amended): A method for the quantitative evaluation of the immune repertoire ~~system~~ of a human individual by analyzing genetic rearrangement of the ~~locus~~ TCRAD locus of said individual ~~as claimed in claim 23~~, which method comprises:

(a) extracting human genomic DNA from a biological sample of said individual, selected from ~~in~~ the group consisting of blood and biopsies;

(b) amplifying multiple different segments ~~a segment~~ of said genomic DNA, resulting from different VJ rearrangements ~~by multiplex long PCR, for detecting, directly in a unique reaction step, several VJ rearrangements of the genes~~ of the ~~locus~~ TCRAD locus ~~said amplifying being~~ ,wherein said amplification is performed by multiplex PCR in the presence:

(i) of one or more pairs of primers, at least one of said pairs of primers consisting of:

- a first primer, called primer V, said primer V hybridizing specifically with a region located upstream of the RSS sequence of a Vx gene to be amplified or with the 5' end of said Vx gene, said Vx gene encoding a V segment of the variable domain of the α chain of a T-cell receptor (TCRAD);

- a second primer, called primer J, said primer J hybridizing specifically with a region located downstream of the RSS sequence of a Jy gene to be amplified, or with the 3' end of said Jy gene to be amplified or in said Jy gene to be amplified, said Jy gene encoding a J segment of the α chain of a T-cell receptor;

(ii) and of a DNA polymerase or a mixture of DNA polymerases for amplifying ~~long~~ genomic DNA segments, and having a correction activity;
said amplification comprising, in addition to the initial denaturation step, cycles of denaturation, hybridization and elongation, in which the elongation steps are carried out at least for 10 minutes at 68°C - 72°C;

(c) ~~the separation of~~ separating the gDNA fragments amplified by electrophoretic migration on a gel, in the presence of a DNA-labeling agent, and

(d) ~~the detection of~~ detecting the rearranged VJ segments ~~by using a DNA-labeling agent during migration, and detecting~~ after excitation in the UV range or at another appropriate wavelength.

Claim 25 (previously presented): The method as claimed in claim 23, wherein in the amplification step (b), the selection of the primers is carried out:

- by systematic analysis of the entire human TCRAD locus using a suitable software,
- selection of the primers whose 3'OH end is complementary only to the region of interest,
- elimination of the primers forming autodimers or stable hairpins, by analysis with a suitable software, and
- elimination of the pairs of primers which form hybrids with one another.

Claim 26 (previously presented): The method as claimed in claim 25, wherein the primers V and J of the pairs of primers V/J are selected from the group consisting of the primers of sequences SEQ ID NO: 1-21.

Claim 27 (previously presented): The method as claimed in claim 23, wherein the amplification step (b) uses additional primers for amplifying, in addition, at least one of the following segments: D segments, V segments and J segments of the TCR β, γ, δ chains and, optionally, segments of the immunoglobulin chains.

Claim 28 (currently amended): The method as claimed in claim 23 or claim 24 wherein, in the amplification step (b), the multiplex ~~long~~ PCR ~~(LPCR)~~ reaction is carried out after purification of the DNA, or directly on a cell lysate.

Claim 29 (previously presented): The method as claimed in claim 23, wherein in the amplification step (b), the elongation steps are incremented by 15-20 seconds per

additional elongation cycle.

Claim 30 (new previously presented The method as claimed in claim 24, wherein step (c) consisting of separation of the amplified DNA fragments by electrophoretic migration on a gel is carried out by pulsed-field migration.

Claim 31 (currently amended): A method for the follow-up to a treatment for a pathology in which the immune system is initially modified, in an individual in need thereof, which method comprises:

- implementing the method ~~for the evaluation of the immune repertoire, as claimed in~~ of claim 24, at the beginning of treatment,

- reiterating said evaluation method at various phases of the treatment, and

- comparing the profile of the immune repertoire ~~system~~ obtained each time with a healthy condition immune repertoire, in order to evaluate the response of said individual to said treatment.

Claim 32 (previously presented): A method for the measurement of the antigen receptor repertoire during the various phases of a pathology in which the immune system is modified, in an individual in need thereof, which method comprises:

- implementing the method for the evaluation of the immune system, as claimed in claim 24 at various phases of the pathology, and

- comparing the profile of the immune system obtained each time with a healthy condition immune repertoire, in order to evaluate the evolution of said pathology.

Claim 33 (currently amended): The method as claimed in claim 24, wherein step(a) is carried out on a biological sample consisting of T lymphocytes from blood or from a biopsy of any origin.

Claim 34 (previously presented): The method as claimed in claim 33, wherein said T lymphocytes are selected from the group consisting of thymic cells, of T lymphocytes from peripheral blood, of T lymphocytes from other lymphoid organs, of T

lymphocytes from various organs and of T lymphocytes derived from tumors or from inflammatory sites.

Claim 35 (previously presented): The method according to claim 23, wherein the size of the segment of amplified gDNA is greater than 10 kb.

Claim 36 (canceled)